

1 **DNA and RNA-SIP reveal Nitrospira spp. as key drivers of**
2 **nitrification in groundwater-fed biofilters**

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Supplementary Table 1

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Table S1-A Genus specific 90% CIs for the change in DNA buoyant density

Comparison	Taxa	90%CI
DNA_C1vsC2	Nitrospira	27.29490368
DNA_C1vsC2	Hyphomicrobium	6.965868301
DNA_C1vsC2	OM27_clade	12.252273
DNA_C1vsC2	Blastocatella	4.527497928
DNA_C1vsC2	Sphingomonas	7.832605989
DNA_C1vsC2	Methyloglobulus	9.972687698
DNA_C1vsC2	Woodsholea	11.51530212
DNA_C1vsC2	uncultured_Latescibacteria_bacterium	4.395130052
DNA_C1vsC2	Pseudomonas	20.78427096
DNA_C1vsC2	Variovorax	3.703893218
DNA_C1vsC2	Nitrosococcus	2.560913888
DNA_C1vsC2	Pedomicrobium	7.954590866
DNA_C1vsC2	uncultured	4.788737221
DNA_C1vsC2	ABS-19	6.385744045
DNA_C1vsC2	Nitrosomonas	2.349722921
DNA_C1vsC2	Rhizobacter	5.251468261
DNA_C1vsC2	CL500-29_marine_group	5.775774936
DNA_C1vsC2	Acidovorax	3.243152628
DNA_C4vsC3	Woodsholea	8.746445583
DNA_C4vsC3	uncultured_Latescibacteria_bacterium	6.922797297
DNA_C4vsC3	Blastocatella	5.900721972
DNA_C4vsC3	ABS_19	4.864921525
DNA_C4vsC3	Sphingomonas	8.427538926
DNA_C4vsC3	Azospira	3.467360657
DNA_C4vsC3	Pedomicrobium	11.24330224
DNA_C4vsC3	Hyphomicrobium	11.25563077
DNA_C4vsC3	Pseudomonas	21.77335039
DNA_C4vsC3	Nitrospira	8.999803853
DNA_C4vsC3	Nitrosomonas	5.042264724
DNA_C4vsC3	Nitrosococcus	2.410856048
DNA_C4vsC3	Methyloglobulus	7.6875397
DNA_C4vsC3	CL500-29_marine_group	10.03613588
DNA_C4vsC3	Acidovorax	6.612988123
DNA_C5vsC6	Woodsholea	34.61995489
DNA_C5vsC6	uncultured_Latescibacteria_bacterium	12.06266939
DNA_C5vsC6	uncultured	7.157708609
DNA_C5vsC6	Sphingomonas	11.87161387
DNA_C5vsC6	Pedomicrobium	27.32630925
DNA_C5vsC6	OM27_clade	35.22452854
DNA_C5vsC6	Nitrospira	69.06265794
DNA_C5vsC6	Nitrosococcus	6.604486979
DNA_C5vsC6	Methyloglobulus	21.34205684
DNA_C5vsC6	Hyphomicrobium	27.3900279
DNA_C5vsC6	CL500-29_marine_group	21.98392165
DNA_C5vsC6	Blastocatella	14.69858365
DNA_C8vsC7	Woodsholea	19.99953085
DNA_C8vsC7	OM27_clade	21.00440171

12 **Table S1 – B** Genus specific 90% CIs for the change in RNA buoyant density

Comparison	Taxa	90%CI
RNA.C1vsC2	Variovorax	0.010946202
RNA.C1vsC2	Methyloglobulus	0.012084529
RNA.C1vsC2	ABS-19	0.009321392
RNA.C1vsC2	CL500-29_marine_group	0.013380092
RNA.C1vsC2	Acidovorax	0.010681521
RNA.C1vsC2	OM27_clade	0.012539093
RNA.C1vsC2	Nitrosococcus	0.010281794
RNA.C1vsC2	Sphingomonas	0.011672409
RNA.C1vsC2	Rhizobacter	0.010244547
RNA.C1vsC2	Woodsholea	0.011844113
RNA.C1vsC2	Pseudomonas	0.010696879
RNA.C1vsC2	uncultured	0.010812986
RNA.C1vsC2	Nitrospira	0.013709626
RNA.C1vsC2	Blastocatella	0.012385466
RNA.C1vsC2	uncultured_Latescibacteria_bacterium	0.009498014
RNA.C1vsC2	Nitrosomonas	0.009555628
RNA.C1vsC2	Pedomicrobium	0.011050473
RNA.C1vsC2	Hyphomicrobium	0.010592564
RNA.C4vsC3	Woodsholea	0.008621579
RNA.C4vsC3	uncultured_Latescibacteria_bacterium	0.007414314
RNA.C4vsC3	Blastocatella	0.00661408
RNA.C4vsC3	ABS_19	0.008422849
RNA.C4vsC3	Sphingomonas	0.007734611
RNA.C4vsC3	Azospira	0.006711897
RNA.C4vsC3	Pedomicrobium	0.007508337
RNA.C4vsC3	Hyphomicrobium	0.00721053
RNA.C4vsC3	Pseudomonas	0.009573882
RNA.C4vsC3	Nitrospira	0.008457103
RNA.C4vsC3	Nitrosomonas	0.006827565
RNA.C4vsC3	Nitrosococcus	0.006299523
RNA.C4vsC3	Methyloglobulus	0.006913547
RNA.C4vsC3	CL500-29_marine_group	0.006162106
RNA.C4vsC3	Acidovorax	0.008380405
RNA.C5vsC6	Woodsholea	0.023065677
RNA.C5vsC6	uncultured_Latescibacteria_bacterium	0.022863257
RNA.C5vsC6	uncultured	0.021014205
RNA.C5vsC6	Sphingomonas	0.022086214
RNA.C5vsC6	Pedomicrobium	0.021504796
RNA.C5vsC6	OM27_clade	0.027101066
RNA.C5vsC6	Nitrospira	0.023046592
RNA.C5vsC6	Nitrosococcus	0.02328091
RNA.C5vsC6	Methyloglobulus	0.02270309
RNA.C5vsC6	Hyphomicrobium	0.020008472
RNA.C5vsC6	CL500-29_marine_group	0.022994518
RNA.C5vsC6	Blastocatella	0.021751132
RNA.C8vsC7	Woodsholea	0.000814697
RNA.C8vsC7	OM27_clade	0.001081158

Table S1-C Blast hits to the putative amoA sequences

Query	Description	Accession	e-value	score
gene_274 GeneMark.hmm 128_aa - 100 486	hypothetical protein [Methyloferula stellata]	gi 519017702 ref WP_020173577.1	2.49E-49	169
gene_238 GeneMark.hmm 188_aa + 2 565	hypothetical protein [Tistlia consotensis]	gi 1184553655 ref WP_085121045.1	2.01E-59	197
gene_284 GeneMark.hmm 159_aa - 152 631	membrane protein [Cupriavidus sp. amp6]	gi 656005008 ref WP_029046450.1	1.20E-37	140
gene_269 GeneMark.hmm 240_aa - 1 720	putative ammonia monooxygenase [Azospirillum brasiliense]	gi 504008002 ref WP_014241996.1	4.71E-43	157
gene_280 GeneMark.hmm 253_aa + 1 759	hypothetical protein [Hyphomicrobium sp. CS1BSMeth3]	gi 1119410285 ref WP_072385832.1	6.52E-72	232
gene_235 GeneMark.hmm 197_aa + 1 594	ammonia monooxygenase [Phyllobacterium sp. YR531]	gi 495398156 ref WP_008122856.1	2.22E-66	215
gene_248 GeneMark.hmm 175_aa - 418 945	hypothetical protein [Ramlibacter sp. Leaf400]	gi 946973621 ref WP_055894610.1	5.07E-52	177
gene_271 GeneMark.hmm 262_aa - 1 786	hypothetical protein [Azospirillum brasiliense]	gi 916533225 ref WP_051140667.1	4.79E-47	168
gene_237 GeneMark.hmm 334_aa - 3 1004	hypothetical protein [Hyphomicrobium sp. CS1BSMeth3]	gi 1119410285 ref WP_072385832.1	4.89E-89	279
gene_260 GeneMark.hmm 238_aa + 2 718	ammonia monooxygenase [Labrenzia alba]	gi 944196777 ref WP_055678338.1	6.67E-46	164
gene_283 GeneMark.hmm 227_aa + 399 1079	hypothetical protein [Azospirillum brasiliense]	gi 916533225 ref WP_051140667.1	2.28E-43	157
gene_202 GeneMark.hmm 328_aa + 575 1558	hypothetical protein [Rhodoplanes sp. Z2-YC6860]	gi 1056597137 ref WP_068028260.1	4.65E-103	315
gene_220 GeneMark.hmm 350_aa - 179 1231	ammonia monooxygenase [Polymorphum gilvum]	gi 503419284 ref WP_013653945.1	7.83E-69	227
gene_205 GeneMark.hmm 291_aa + 809 1681	hypothetical protein [Caldimonas taiwanensis]	gi 1180938568 ref WP_084362242.1	6.46E-80	254
gene_200 GeneMark.hmm 368_aa - 567 1673	hypothetical protein [Rhodoplanes sp. Z2-YC6860]	gi 1056597137 ref WP_068028260.1	6.38E-105	321
gene_197 GeneMark.hmm 368_aa + 44 1150	hypothetical protein [Rhodoplanes sp. Z2-YC6860]	gi 1056597137 ref WP_068028260.1	6.38E-105	321
gene_217 GeneMark.hmm 311_aa - 636 1571	membrane protein [Pseudogulbenkiania sp. MAI-1]	gi 635657271 ref WP_024304138.1	1.23E-75	243
gene_223 GeneMark.hmm 380_aa - 341 1483	hypothetical protein [Hyphomicrobium sp. CS1BSMeth3]	gi 1119410285 ref WP_072385832.1	3.60E-127	378
gene_227 GeneMark.hmm 366_aa - 1878 2978	hypothetical protein [Hyphomicrobium sp. CS1BSMeth3]	gi 1119410285 ref WP_072385832.1	7.66E-127	377
gene_287 GeneMark.hmm 248_aa - 2178 2924	hypothetical protein [Rhizobiales bacterium CCH3-A5]	gi 1177645899 ref WP_082736595.1	2.94E-80	253
gene_268 GeneMark.hmm 287_aa - 2379 3242	ammonia monooxygenase [Rhizobium sp. NT-26]	gi 918947167 ref WP_052641815.1	3.31E-36	140
gene_209 GeneMark.hmm 352_aa + 2469 3527	membrane protein [Pseudogulbenkiania sp. MAI-1]	gi 635657271 ref WP_024304138.1	1.14E-83	265
gene_257 GeneMark.hmm 292_aa - 3418 4296	ammonia monooxygenase [Rhizobium sp. NT-26]	gi 918947167 ref WP_052641815.1	9.85E-38	144
gene_179 GeneMark.hmm 368_aa - 4069 5175	hypothetical protein [Rhodoplanes sp. Z2-YC6860]	gi 1056597137 ref WP_068028260.1	8.96E-108	328
gene_277 GeneMark.hmm 271_aa + 1 816	AbrB family transcriptional regulator [Thauera sp. 27]	gi 489025714 ref WP_002936124.1	3.73E-39	148
gene_233 GeneMark.hmm 350_aa + 5216 6268	ammonia monooxygenase [Polymorphum gilvum]	gi 503419284 ref WP_013653945.1	4.94E-67	223
gene_246 GeneMark.hmm 318_aa + 6379 7335	ammonia monooxygenase [Azorhizobium caulinodans]	gi 501122003 ref WP_012171155.1	1.60E-48	174
gene_196 GeneMark.hmm 336_aa - 14681 15691	membrane protein [Pseudogulbenkiania sp. MAI-1]	gi 635657271 ref WP_024304138.1	1.58E-85	270
gene_124 GeneMark.hmm 359_aa + 83125 84204	hypothetical protein [Variovorax paradoxus]	gi 951108200 ref WP_057597630.1	1.15E-103	317
gene_35 GeneMark.hmm 359_aa - 30096 31175	hypothetical protein [Variovorax paradoxus]	gi 951108200 ref WP_057597630.1	1.15E-103	317